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SEQUENCE LISTING

<110> DANA-FARBER CANCER INSTITUTE

<120> LYMPHOMA ASSOCIATED MOLECULES AND USES THEREFOR

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<150> USSN 60/106,383

<151> 1998-10-29

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<170> PatentIn Ver. 2.0

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Thr Ser Leu Ser Leu Leu Phe Gln Lys Val Phe Ala Gln Ile Phe Pro
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1293

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Ile Phe Pro Thr Asp Leu Glu Ile Tyr Lys Ala Phe Ser Ser Glu Met

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 Pro Tyr Gln Phe Cys Asn Val Val Cys Arg Val Gly Phe Gln Arg Met
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- 6 -

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Pro Val Asp

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2890

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Ile Ile His Ala Val Gly Pro Arg Trp Met Glu Trp Asp Lys Gln Gly 195 200 205		
Cys Thr Gly Lys Leu Gln Arg Ala Ile Val Ser Ile Leu Asn Tyr Val 210 215 220		
Ile Tyr Lys Asn Thr His Ile Lys Thr Val Ala Ile Pro Ala Leu Ser 225 230 235 240		
Ser Gly Ile Phe Gln Phe Pro Leu Asn Leu Cys Thr Lys Thr Ile Val 245 250 255		
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Lys Glu Ile His Leu Val Ser Asn Glu Asp Pro Thr Val Ala Ala Phe 275 280 285		
Lys Ala Ala Ser Glu Phe Ile Leu Gly Lys Ser Glu Leu Gly Gln Glu 290 295 300		
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Ser Val Asn Pro His Asp Ile Thr Val Gly Pro Val Ala Lys Ser Ile 340 345 350		
Leu Gln Gln Ala Gly Val Glu Met Lys Ser Glu Phe Leu Ala Thr Lys 355 360 365		
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Asn Leu Phe Cys Lys Tyr Ile Tyr His Val Leu Trp His Ser Glu Phe 385 390 395 400		
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Cys Ile Glu Gln Asn Ile Thr Ser Ile Ser Phe Pro Ala Leu Gly Thr 420 425 430		
Gly Asn Met Glu Ile Lys Lys Glu Thr Ala Ala Glu Ile Leu Phe Asp 435 440 445		

- 8 -

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 Tyr Phe Thr Lys Asn Leu Lys Asn Leu Ala Glu Lys Ala Lys Lys Ile
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- 10 -

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Lys	Ala	Ala	Ser	Glu	Phe	Ile	Leu	Gly	Lys	Ser	Glu	Leu	Gly	Gln	Glu															
		290				295					300																			
acc	acc	cct	tct	ttc	aat	gca	atg	gtc	gtg	aac	aac	ctg	acc	ctc	cag	960														
Thr	Thr	Pro	Ser	Phe	Asn	Ala	Met	Val	Val	Asn	Asn	Leu	Thr	Leu	Gln															
		305			310					315				320																
att	gtc	cag	ggc	cac	att	gaa	tgg	cag	acg	gca	gat	gta	att	gtt	aat															
1008																														
Ile	Val	Gln	Gly	His	Ile	Glu	Trp	Gln	Thr	Ala	Asp	Val	Ile	Val	Asn															
				325					330					335																

- 11 -

tct gta aac cca cat gat att aca gtt gga cct gtg gca aag tca att
1056

Ser Val Asn Pro His Asp Ile Thr Val Gly Pro Val Ala Lys Ser Ile
340 345 350

cta caa caa gca gga gtt gaa atg aaa tcg gaa ttt ctt gcc aca aag
1104

Leu Gln Gln Ala Gly Val Glu Met Lys Ser Glu Phe Leu Ala Thr Lys
355 360 365

gct aaa cag ttt caa cgg tcc cag ttg gta ctg gtc aca aaa gga ttt
1152

Ala Lys Gln Phe Gln Arg Ser Gln Leu Val Leu Val Thr Lys Gly Phe
370 375 380

aac ttg ttc tgt aaa tat ata tac cat gta ctg tgg cat tca gaa ttt
1200

Asn Leu Phe Cys Lys Tyr Ile Tyr His Val Leu Trp His Ser Glu Phe
385 390 395 400

cct aaa cct cag ata tta aaa cat gca atg aag gag tgt ttg gaa aaa
1248

Pro Lys Pro Gln Ile Leu Lys His Ala Met Lys Glu Cys Leu Glu Lys
405 410 415

tgc att gag caa aat ata act tcc att tcc ttt cct gcc ctt ggg act
1296

Cys Ile Glu Gln Asn Ile Thr Ser Ile Ser Phe Pro Ala Leu Gly Thr
420 425 430

gga aac atg gaa ata aag aag gaa aca gca gca gag att ttg ttt gat
1344

Gly Asn Met Glu Ile Lys Lys Glu Thr Ala Ala Glu Ile Leu Phe Asp
435 440 445

gaa gtt tta aca ttt gcc aaa gac cat gta aaa cac cag tta act gta
1392

Glu Val Leu Thr Phe Ala Lys Asp His Val Lys His Gln Leu Thr Val
450 455 460

aaa ttt gtg atc ttt cca aca gat ttg gag ata tat aag gct ttc agt
1440

Lys Phe Val Ile Phe Pro Thr Asp Leu Glu Ile Tyr Lys Ala Phe Ser
465 470 475 480

tct gaa atg gca aag agg tcc aag atg ctg agt ttg aac aat tac agt
1488

Ser Glu Met Ala Lys Arg Ser Lys Met Leu Ser Leu Asn Asn Tyr Ser
485 490 495

gtc ccc cag tca acc aga gag gag aaa aga gaa aat ggg ctt gaa gct
1536

Val Pro Gln Ser Thr Arg Glu Glu Lys Arg Glu Asn Gly Leu Glu Ala
500 505 510

aga tct cct gcc atc aat ctg atg gga ttc aac gtg gaa gag atg tat

- 12 -

1584

Arg Ser Pro Ala Ile Asn Leu Met Gly Phe Asn Val Glu Glu Met Tyr
 515 520 525

gag gcc cac gca tgg atc caa aga atc ctg agt ctc cag aac cac cac
 1632

Glu Ala His Ala Trp Ile Gln Arg Ile Leu Ser Leu Gln Asn His His
 530 535 540

atc att gag aat aat cat att ctg tac ctt ggg aga aag gaa cat gac
 1680

Ile Ile Glu Asn Asn His Ile Leu Tyr Leu Gly Arg Lys Glu His Asp
 545 550 555 560

att ttg tct cag ctt cag aaa act tca agt gtc tcc atc aca gaa att
 1728

Ile Leu Ser Gln Leu Gln Lys Thr Ser Ser Val Ser Ile Thr Glu Ile
 565 570 575

atc agc cca gga agg aca gag tta gag att gaa gga gcc cgg gct gac
 1776

Ile Ser Pro Gly Arg Thr Glu Leu Glu Ile Glu Gly Ala Arg Ala Asp
 580 585 590

ctc att gag gtg gtt atg aac att gaa gat atg ctt tgt aaa gta cag
 1824

Leu Ile Glu Val Val Met Asn Ile Glu Asp Met Leu Cys Lys Val Gln
 595 600 605

gag gaa atg gca agg aaa aag gag cga ggc ctt tgg cgc tcg tta gga
 1872

Glu Glu Met Ala Arg Lys Lys Glu Arg Gly Leu Trp Arg Ser Leu Gly
 610 615 620

cag tgg act att cag caa caa aaa acc caa gac gaa atg aaa gaa aat
 1920

Gln Trp Thr Ile Gln Gln Gln Lys Thr Gln Asp Glu Met Lys Glu Asn
 625 630 635 640

atc ata ttt ctg aaa tgt cct gtg cct cca act caa gag ctt cta gat
 1968

Ile Ile Phe Leu Lys Cys Pro Val Pro Pro Thr Gln Glu Leu Leu Asp
 645 650 655

caa aag aaa cag ttt gaa aaa tgt ggt ttg cag gtt cta aag gtg gag
 2016

Gln Lys Lys Gln Phe Glu Lys Cys Gly Leu Gln Val Leu Lys Val Glu
 660 665 670

aag ata gac aat gag gtc ctt atg gct gcc ttt caa aga aag aag aaa
 2064

Lys Ile Asp Asn Glu Val Leu Met Ala Ala Phe Gln Arg Lys Lys Lys
 675 680 685

atg atg gaa gaa aaa ctg cac agg caa cct gtg agc cat agg ctg ttt
 2112

Met Met Glu Glu Lys Leu His Arg Gln Pro Val Ser His Arg Leu Phe
 690 695 700

1584
1632
1680
1728
1776
1824
1872
1920
1968
2016
2064
2112

- 13 -

cag caa gtc cca tac cag ttc tgc aat gtg gta tgc aga gtt ggc ttt
2160

Gln Gln Val Pro Tyr Gln Phe Cys Asn Val Val Cys Arg Val Gly Phe
705 710 715 720

caa aga atg tac tcg aca cct tgc gat cca aaa tac gga gct ggc ata
2208

Gln Arg Met Tyr Ser Thr Pro Cys Asp Pro Lys Tyr Gly Ala Gly Ile
725 730 735

tac ttc acc aag aac ctc aaa aac ctg gca gag aag gcc aag aaa atc
2256

Tyr Phe Thr Lys Asn Leu Lys Asn Leu Ala Glu Lys Ala Lys Lys Ile
740 745 750

tct gct gca gat aag ctg atc tat gtg ttt gag gct gaa gta ctc acà
2304

Ser Ala Ala Asp Lys Leu Ile Tyr Val Phe Glu Ala Glu Val Leu Thr
755 760 765

ggc ttc ttc tgc cag gga cat ccg tta aat att gtt ccc cca cca ctg
2352

Gly Phe Phe Cys Gln Gly His Pro Leu Asn Ile Val Pro Pro Pro Leu
770 775 780

agt cct gga gct ata gat ggt cat gac agt gtg gtt gac aat gtc tcc
2400

Ser Pro Gly Ala Ile Asp Gly His Asp Ser Val Val Asp Asn Val Ser
785 790 795 800

agc cct gaa acc ttt gtt att ttt agt ggc atg cag gct ata cct cag
2448

Ser Pro Glu Thr Phe Val Ile Phe Ser Gly Met Gln Ala Ile Pro Gln
805 810 815

tat ttg tgg aca tgc acc cag gaa tat gta cag tca caa gat tac tca
2496

Tyr Leu Trp Thr Cys Thr Gln Glu Tyr Val Gln Ser Gln Asp Tyr Ser
820 825 830

tca gga cca atg aga ccc ttt gca cag cat cct tgg agg gga ttc gca
2544

Ser Gly Pro Met Arg Pro Phe Ala Gln His Pro Trp Arg Gly Phe Ala
835 840 845

agt ggc agc cct gtt gat
2562

Ser Gly Ser Pro Val Asp
850

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<211> 3024

<212> DNA

<213> Murinae gen. sp.

<220>

- 14 -

<221> CDS

<222> (171)..(2648)

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gaatagaggg aaacaggcca ccattctctc gatctacaga ctacacttgg aaacacaaac 120

aaatataaat atctgaagac ccacgtggga cctgaagaat ggccctattac atg gat 176
 Met Asp
 1

aca tgg gcg gca gct ccc gcc gaa aga cca gcc aac aat tct ctt gaa 224
 Thr Trp Ala Ala Ala Pro Ala Glu Arg Pro Ala Asn Asn Ser Leu Glu
 5 10 15

gaa cat tat aga tgg caa att ccc att aaa cac aat gtc ttc gaa att 272
 Glu His Tyr Arg Trp Gln Ile Pro Ile Lys His Asn Val Phe Glu Ile
 20 25 30

tta aag agc aat gag agt cag cta tgt gaa gtc ctc caa aat aag ttt 320
 Leu Lys Ser Asn Glu Ser Gln Leu Cys Glu Val Leu Gln Asn Lys Phe
 35 40 45 50

gga tgc atc tct acc ctg agc tgt cca act cta gca ggg agc agc tct 368
 Gly Cys Ile Ser Thr Leu Ser Cys Pro Thr Leu Ala Gly Ser Ser Ser
 55 60 65

cct gct cag aga gtc ttc aga agg acc ctg atc cct ggg ata gag tta 416
 Pro Ala Gln Arg Val Phe Arg Arg Thr Leu Ile Pro Gly Ile Glu Leu
 70 75 80

tct gtc tgg aag gat gac ctt acc aga cac gtt gtt gat gct gtg gtg 464
 Ser Val Trp Lys Asp Asp Leu Thr Arg His Val Val Asp Ala Val Val
 85 90 95

aac gca gcc aat gaa aac ctt ttg cat gga agt ggc ctg gcc gga agc 512
 Asn Ala Ala Asn Glu Asn Leu Leu His Gly Ser Gly Leu Ala Gly Ser
 100 105 110

ttg gtg aaa act ggt ggc ttt gaa atc caa gaa gag agc aaa aga atc 560
 Leu Val Lys Thr Gly Gly Phe Glu Ile Gln Glu Glu Ser Lys Arg Ile
 115 120 125 130

att gcc aac gtt ggt aaa atc tca gtt ggt gga atc gct atc acc ggt 608
 Ile Ala Asn Val Gly Lys Ile Ser Val Gly Gly Ile Ala Ile Thr Gly
 135 140 145

gcg ggg aga ctt cct tgc cat ttg att atc cat gcg gtt gga cct cgg 656
 Ala Gly Arg Leu Pro Cys His Leu Ile Ile His Ala Val Gly Pro Arg
 150 155 160

tgg aca gtt acg aac agc cag aca gct atc gaa tta ctg aaa ttt gcc 704
 Trp Thr Val Thr Asn Ser Gln Thr Ala Ile Glu Leu Leu Lys Phe Ala
 165 170 175

att agg aac att cta gat tat gtc acc aaa tat gat cta cgc att aag 752
 Ile Arg Asn Ile Leu Asp Tyr Val Thr Lys Tyr Asp Leu Arg Ile Lys

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180	185	190	
aca gta gca att cca gcc ctg agc tct gga att ttc cag ttc cct ctg			800
Thr Val Ala Ile Pro Ala Leu Ser Ser Gly Ile Phe Gln Phe Pro Leu			
195	200	205	210
gat ttg tgt aca agc ata att tta gaa act atc cgg ctt tat ttc caa			848
Asp Leu Cys Thr Ser Ile Ile Leu Glu Thr Ile Arg Leu Tyr Phe Gln			
	215	220	225
gac aag caa atg ttc ggt aat ttg aga gag att cat ctg gtg agc aat			896
Asp Lys Gln Met Phe Gly Asn Leu Arg Glu Ile His Leu Val Ser Asn			
	230	235	240
gag gac ccc act gtt gcg tcc ttt aaa tcc gcc tca gaa agc atc cta			944
Glu Asp Pro Thr Val Ala Ser Phe Lys Ser Ala Ser Glu Ser Ile Leu			
	245	250	255
ggg agg gac ctg agc tct tgg ggg ggt cca gaa act gac cct gct tcc			992
Gly Arg Asp Leu Ser Ser Trp Gly Gly Pro Glu Thr Asp Pro Ala Ser			
	260	265	270
acc atg act ctt cgc atc ggc cgg ggc ctg act ctc cag att gtc caa			
1040			
Thr Met Thr Leu Arg Ile Gly Arg Gly Leu Thr Leu Gln Ile Val Gln			
275	280	285	290
ggc tgt att gaa atg caa aca aca gat gta att ggt aat tct gga tac			
1088			
Gly Cys Ile Glu Met Gln Thr Thr Asp Val Ile Gly Asn Ser Gly Tyr			
	295	300	305
atg cag gat ttt aaa tca gga cga gtg gca cag tcg att ctt aga caa			
1136			
Met Gln Asp Phe Lys Ser Gly Arg Val Ala Gln Ser Ile Leu Arg Gln			
	310	315	320
gca ggg gtt gaa atg gaa aag gaa ctt gac aag gtt aac ctg tcc aca			
1184			
Ala Gly Val Glu Met Glu Lys Glu Leu Asp Lys Val Asn Leu Ser Thr			
	325	330	335
gat tat caa gag gtg tgg gtc aca aaa gga ttt aaa ttg tcc tgt cag			
1232			
Asp Tyr Gln Glu Val Trp Val Thr Lys Gly Phe Lys Leu Ser Cys Gln			
	340	345	350
tat gtc ttc cat gtg gca tgg cat tcc caa atc aac aaa tac cag ata			
1280			
Tyr Val Phe His Val Ala Trp His Ser Gln Ile Asn Lys Tyr Gln Ile			
355	360	365	370
ttg aaa gat gca atg aag tcc tgt cta gaa aaa tgc ctt aaa cca gat			
1328			
Leu Lys Asp Ala Met Lys Ser Cys Leu Glu Lys Cys Leu Lys Pro Asp			
	375	380	385
ata aat tcc att tcc ttt cct gct ctc ggg aca gga ttg atg gat ttg			

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1376

Ile Asn Ser Ile Ser Phe Pro Ala Leu Gly Thr Gly Leu Met Asp Leu
 390 395 400

aag aag agt aca gca gct cag ata atg ttt gag gaa gtt ttt gca ttt
 1424

Lys Lys Ser Thr Ala Ala Gln Ile Met Phe Glu Glu Val Phe Ala Phe
 405 410 415

gct aaa gag cac aag gaa aaa acg cta act gta aag att gtg atc ttt
 1472

Ala Lys Glu His Lys Glu Lys Thr Leu Thr Val Lys Ile Val Ile Phe
 420 425 430

cca gta gat gtg gag acg tac aag att ttt tat gct gaa atg aca aaa
 1520

Pro Val Asp Val Glu Thr Tyr Lys Ile Phe Tyr Ala Glu Met Thr Lys
 435 440 445 450

agg tcc aac gag ctg aat ctc agc ggt aat agt ggt gct tta gcc ctg
 1568

Arg Ser Asn Glu Leu Asn Leu Ser Gly Asn Ser Gly Ala Leu Ala Leu
 455 460 465

cag tgg tcc agt ggg gag caa aga aga ggc ggc ctt gaa gct gga tct
 1616

Gln Trp Ser Ser Gly Glu Gln Arg Arg Gly Gly Leu Glu Ala Gly Ser
 470 475 480

cct gcc atc aat ctc atg ggt gta aaa gtg gga gag atg tgt gag gcc
 1664

Pro Ala Ile Asn Leu Met Gly Val Lys Val Gly Glu Met Cys Glu Ala
 485 490 495

cag gaa tgg att gaa agg ttg ctg gtc tcc ctg gac cac cac atc att
 1712

Gln Glu Trp Ile Glu Arg Leu Leu Val Ser Leu Asp His His Ile Ile
 500 505 510

gag aat aat cat att ctc tat ctt ggg aaa aaa gag cac gac gtg ctg
 1760

Glu Asn Asn His Ile Leu Tyr Leu Gly Lys Lys Glu His Asp Val Leu
 515 520 525 530

tct gag ctc cag acc agc aca aga gtc tcc att tca gag act gtc agt
 1808

Ser Glu Leu Gln Thr Ser Thr Arg Val Ser Ile Ser Glu Thr Val Ser
 535 540 545

cca aga acg gcc act ttg gag att aaa ggt ccc cag gct gac ctc att
 1856

Pro Arg Thr Ala Thr Leu Glu Ile Lys Gly Pro Gln Ala Asp Leu Ile
 550 555 560

gac gca gtt atg agg att gaa tgt atg ctg tgt gac gtt cag gaa gaa
 1904

Asp Ala Val Met Arg Ile Glu Cys Met Leu Cys Asp Val Gln Glu Glu
 565 570 575

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gtg gca gga aaa agg gag aaa aat ctt tgg agc ttg tca gga cag ggg
1952

Val Ala Gly Lys Arg Glu Lys Asn Leu Trp Ser Leu Ser Gly Gln Gly
580 585 590

acc aac cag caa gaa aaa ctg gat aaa atg gaa gaa tcg tac aca ttt
2000

Thr Asn Gln Gln Glu Lys Leu Asp Lys Met Glu Glu Ser Tyr Thr Phe
595 600 605 610

caa cga tac cca gca tca tta act cag gaa ctt cag gac cga aag aaa
2048

Gln Arg Tyr Pro Ala Ser Leu Thr Gln Glu Leu Gln Asp Arg Lys Lys
615 620 625

cag ttt gaa aag tgt ggc ttg tgg gtt gtg cag gtg gag cag ata gac
2096

Gln Phe Glu Lys Cys Gly Leu Trp Val Val Gln Val Glu Gln Ile Asp
630 635 640

aat aag gtg ctg ctg gct gcc ttc caa gag aag aag aaa atg atg gaa
2144

Asn Lys Val Leu Leu Ala Ala Phe Gln Glu Lys Lys Lys Met Met Glu
645 650 655

gag agg acg cca aag gga tct ggg agc caa agg ttg ttt cag cag gtc
2192

Glu Arg Thr Pro Lys Gly Ser Gly Ser Gln Arg Leu Phe Gln Gln Val
660 665 670

cca cat cag ttc tgc aat acg gtg tgc aga gtc ggc ttc cac aga atg
2240

Pro His Gln Phe Cys Asn Thr Val Cys Arg Val Gly Phe His Arg Met
675 680 685 690

tat tcg aca tcc tat aac cca gtt tat gga gcc ggc ata tat ttc acc
2288

Tyr Ser Thr Ser Tyr Asn Pro Val Tyr Gly Ala Gly Ile Tyr Phe Thr
695 700 705

aag agc ctc aaa aat cta gca gac aag gtc aag aaa acc tca agc aca
2336

Lys Ser Leu Lys Asn Leu Ala Asp Lys Val Lys Lys Thr Ser Ser Thr
710 715 720

gac aag cta atc tat gtg ttt gag gca gaa gta ctc aca ggg tcc ttc
2384

Asp Lys Leu Ile Tyr Val Phe Glu Ala Glu Val Leu Thr Gly Ser Phe
725 730 735

tgt cag ggt aat tcc tca aat atc atc cct cca cca ttg agt cct ggg
2432

Cys Gln Gly Asn Ser Ser Asn Ile Ile Pro Pro Pro Leu Ser Pro Gly
740 745 750

gcc tta gat gtc aat gac agc gta gtt gac aat gtt tcc agc cct gaa
2480

- 18 -

Ala Leu Asp Val Asn Asp Ser Val Val Asp Asn Val Ser Ser Pro Glu
755 760 765 770

acc att gtt gtt ttt aat ggc atg cag gcc atg ccc ctg tac ttg tgg
2528

Thr Ile Val Val Phe Asn Gly Met Gln Ala Met Pro Leu Tyr Leu Trp
775 780 785

act tgc aca cag gat agg aca ttc tca cag cat ccg atg tgg tca cag
2576

Thr Cys Thr Gln Asp Arg Thr Phe Ser Gln His Pro Met Trp Ser Gln
790 795 800

gac tac tca tca gga cca gga atg gtc tct tcg ctg cag tcc tgg gaa
2624

Asp Tyr Ser Ser Gly Pro Gly Met Val Ser Ser Leu Gln Ser Trp Glu
805 810 815

tgg gtc tta aat ggc agc tct gtt tagtgtctac atcagtttaa caagcagaag
2678

Trp Val Leu Asn Gly Ser Ser Val
820 825

gggttgagag aactgacaaa atgataaata acagggttacc tgttcagaat gatgggggtca
2738

ctaaaggcac cgaccacaca ctagcatcat agtgcctttg tctttacctc tgggcttgac
2798

tgggcagatg ccagctaaaa ctctctcaact gtcttttcta tttgacatct ttcattctct
2858

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2918

tattttctaa aatgatagca caaactagga caacaggatg atttcagggtt ttctatataa
2978

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3024

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<212> PRT

<213> Murinae gen. sp.

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20 25 30

Glu Ile Leu Lys Ser Asn Glu Ser Gln Leu Cys Glu Val Leu Gln Asn
35 40 45

Lys Phe Gly Cys Ile Ser Thr Leu Ser Cys Pro Thr Leu Ala Gly Ser

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50					55					60					
Ser	Ser	Pro	Ala	Gln	Arg	Val	Phe	Arg	Arg	Thr	Leu	Ile	Pro	Gly	Ile
65					70					75					80
Glu	Leu	Ser	Val	Trp	Lys	Asp	Asp	Leu	Thr	Arg	His	Val	Val	Asp	Ala
				85					90					95	
Val	Val	Asn	Ala	Ala	Asn	Glu	Asn	Leu	Leu	His	Gly	Ser	Gly	Leu	Ala
			100					105					110		
Gly	Ser	Leu	Val	Lys	Thr	Gly	Gly	Phe	Glu	Ile	Gln	Glu	Glu	Ser	Lys
		115					120					125			
Arg	Ile	Ile	Ala	Asn	Val	Gly	Lys	Ile	Ser	Val	Gly	Gly	Ile	Ala	Ile
	130					135					140				
Thr	Gly	Ala	Gly	Arg	Leu	Pro	Cys	His	Leu	Ile	Ile	His	Ala	Val	Gly
145					150					155					160
Pro	Arg	Trp	Thr	Val	Thr	Asn	Ser	Gln	Thr	Ala	Ile	Glu	Leu	Leu	Lys
				165					170					175	
Phe	Ala	Ile	Arg	Asn	Ile	Leu	Asp	Tyr	Val	Thr	Lys	Tyr	Asp	Leu	Arg
			180					185					190		
Ile	Lys	Thr	Val	Ala	Ile	Pro	Ala	Leu	Ser	Ser	Gly	Ile	Phe	Gln	Phe
		195					200					205			
Pro	Leu	Asp	Leu	Cys	Thr	Ser	Ile	Ile	Leu	Glu	Thr	Ile	Arg	Leu	Tyr
	210					215					220				
Phe	Gln	Asp	Lys	Gln	Met	Phe	Gly	Asn	Leu	Arg	Glu	Ile	His	Leu	Val
225					230					235					240
Ser	Asn	Glu	Asp	Pro	Thr	Val	Ala	Ser	Phe	Lys	Ser	Ala	Ser	Glu	Ser
				245					250					255	
Ile	Leu	Gly	Arg	Asp	Leu	Ser	Ser	Trp	Gly	Gly	Pro	Glu	Thr	Asp	Pro
			260					265					270		
Ala	Ser	Thr	Met	Thr	Leu	Arg	Ile	Gly	Arg	Gly	Leu	Thr	Leu	Gln	Ile
		275					280					285			
Val	Gln	Gly	Cys	Ile	Glu	Met	Gln	Thr	Thr	Asp	Val	Ile	Gly	Asn	Ser
	290					295					300				
Gly	Tyr	Met	Gln	Asp	Phe	Lys	Ser	Gly	Arg	Val	Ala	Gln	Ser	Ile	Leu
305					310					315					320
Arg	Gln	Ala	Gly	Val	Glu	Met	Glu	Lys	Glu	Leu	Asp	Lys	Val	Asn	Leu
				325					330					335	
Ser	Thr	Asp	Tyr	Gln	Glu	Val	Trp	Val	Thr	Lys	Gly	Phe	Lys	Leu	Ser
			340					345					350		
Cys	Gln	Tyr	Val	Phe	His	Val	Ala	Trp	His	Ser	Gln	Ile	Asn	Lys	Tyr
		355					360					365			

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Gln Ile Leu Lys Asp Ala Met Lys Ser Cys Leu Glu Lys Cys Leu Lys
 370 375 380
 Pro Asp Ile Asn Ser Ile Ser Phe Pro Ala Leu Gly Thr Gly Leu Met
 385 390 395 400
 Asp Leu Lys Lys Ser Thr Ala Ala Gln Ile Met Phe Glu Glu Val Phe
 405 410 415
 Ala Phe Ala Lys Glu His Lys Glu Lys Thr Leu Thr Val Lys Ile Val
 420 425 430
 Ile Phe Pro Val Asp Val Glu Thr Tyr Lys Ile Phe Tyr Ala Glu Met
 435 440 445
 Thr Lys Arg Ser Asn Glu Leu Asn Leu Ser Gly Asn Ser Gly Ala Leu
 450 455 460
 Ala Leu Gln Trp Ser Ser Gly Glu Gln Arg Arg Gly Gly Leu Glu Ala
 465 470 475 480
 Gly Ser Pro Ala Ile Asn Leu Met Gly Val Lys Val Gly Glu Met Cys
 485 490 495
 Glu Ala Gln Glu Trp Ile Glu Arg Leu Leu Val Ser Leu Asp His His
 500 505 510
 Ile Ile Glu Asn Asn His Ile Leu Tyr Leu Gly Lys Lys Glu His Asp
 515 520 525
 Val Leu Ser Glu Leu Gln Thr Ser Thr Arg Val Ser Ile Ser Glu Thr
 530 535 540
 Val Ser Pro Arg Thr Ala Thr Leu Glu Ile Lys Gly Pro Gln Ala Asp
 545 550 555 560
 Leu Ile Asp Ala Val Met Arg Ile Glu Cys Met Leu Cys Asp Val Gln
 565 570 575
 Glu Glu Val Ala Gly Lys Arg Glu Lys Asn Leu Trp Ser Leu Ser Gly
 580 585 590
 Gln Gly Thr Asn Gln Gln Glu Lys Leu Asp Lys Met Glu Glu Ser Tyr
 595 600 605
 Thr Phe Gln Arg Tyr Pro Ala Ser Leu Thr Gln Glu Leu Gln Asp Arg
 610 615 620
 Lys Lys Gln Phe Glu Lys Cys Gly Leu Trp Val Val Gln Val Glu Gln
 625 630 635 640
 Ile Asp Asn Lys Val Leu Leu Ala Ala Phe Gln Glu Lys Lys Lys Met
 645 650 655
 Met Glu Glu Arg Thr Pro Lys Gly Ser Gly Ser Gln Arg Leu Phe Gln
 660 665 670

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Gln Val Pro His Gln Phe Cys Asn Thr Val Cys Arg Val Gly Phe His
675 680 685

Arg Met Tyr Ser Thr Ser Tyr Asn Pro Val Tyr Gly Ala Gly Ile Tyr
690 695 700

Phe Thr Lys Ser Leu Lys Asn Leu Ala Asp Lys Val Lys Lys Thr Ser
705 710 715 720

Ser Thr Asp Lys Leu Ile Tyr Val Phe Glu Ala Glu Val Leu Thr Gly
725 730 735

Ser Phe Cys Gln Gly Asn Ser Ser Asn Ile Ile Pro Pro Pro Leu Ser
740 745 750

Pro Gly Ala Leu Asp Val Asn Asp Ser Val Val Asp Asn Val Ser Ser
755 760 765

Pro Glu Thr Ile Val Val Phe Asn Gly Met Gln Ala Met Pro Leu Tyr
770 775 780

Leu Trp Thr Cys Thr Gln Asp Arg Thr Phe Ser Gln His Pro Met Trp
785 790 795 800

Ser Gln Asp Tyr Ser Ser Gly Pro Gly Met Val Ser Ser Leu Gln Ser
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Trp Glu Trp Val Leu Asn Gly Ser Ser Val
820 825

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<213> Murinae gen. sp.

<220>

<221> CDS

<222> (1)..(2478)

<400> 6

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ctt gaa gaa cat tat aga tgg caa att ccc att aaa cac aat gtc ttc 96

Leu Glu Glu His Tyr Arg Trp Gln Ile Pro Ile Lys His Asn Val Phe
20 25 30

gaa att tta aag agc aat gag agt cag cta tgt gaa gtc ctc caa aat 144

Glu Ile Leu Lys Ser Asn Glu Ser Gln Leu Cys Glu Val Leu Gln Asn
35 40 45

aag ttt gga tgc atc tct acc ctg agc tgt cca act cta gca ggg agc 192

Lys Phe Gly Cys Ile Ser Thr Leu Ser Cys Pro Thr Leu Ala Gly Ser
50 55 60

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agc tct cct gct cag aga gtc ttc aga agg acc ctg atc cct ggg ata	240
Ser Ser Pro Ala Gln Arg Val Phe Arg Arg Thr Leu Ile Pro Gly Ile	
65 70 75 80	
gag tta tct gtc tgg aag gat gac ctt acc aga cac gtt gtt gat gct	288
Glu Leu Ser Val Trp Lys Asp Asp Leu Thr Arg His Val Val Asp Ala	
85 90 95	
gtg gtg aac gca gcc aat gaa aac ctt ttg cat gga agt ggc ctg gcc	336
Val Val Asn Ala Ala Asn Glu Asn Leu Leu His Gly Ser Gly Leu Ala	
100 105 110	
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Gly Ser Leu Val Lys Thr Gly Gly Phe Glu Ile Gln Glu Glu Ser Lys	
115 120 125	
aga atc att gcc aac gtt ggt aaa atc tca gtt ggt gga atc gct atc	432
Arg Ile Ile Ala Asn Val Gly Lys Ile Ser Val Gly Gly Ile Ala Ile	
130 135 140	
acc ggt gcg ggg aga ctt cct tgc cat ttg att atc cat gcg gtt gga	480
Thr Gly Ala Gly Arg Leu Pro Cys His Leu Ile Ile His Ala Val Gly	
145 150 155 160	
cct cgg tgg aca gtt acg aac agc cag aca gct atc gaa tta ctg aaa	528
Pro Arg Trp Thr Val Thr Asn Ser Gln Thr Ala Ile Glu Leu Leu Lys	
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Phe Ala Ile Arg Asn Ile Leu Asp Tyr Val Thr Lys Tyr Asp Leu Arg	
180 185 190	
att aag aca gta gca att cca gcc ctg agc tct gga att ttc cag ttc	624
Ile Lys Thr Val Ala Ile Pro Ala Leu Ser Ser Gly Ile Phe Gln Phe	
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cct ctg gat ttg tgt aca agc ata att tta gaa act atc cgg ctt tat	672
Pro Leu Asp Leu Cys Thr Ser Ile Ile Leu Glu Thr Ile Arg Leu Tyr	
210 215 220	
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Phe Gln Asp Lys Gln Met Phe Gly Asn Leu Arg Glu Ile His Leu Val	
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Ser Asn Glu Asp Pro Thr Val Ala Ser Phe Lys Ser Ala Ser Glu Ser	
245 250 255	
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Ile Leu Gly Arg Asp Leu Ser Ser Trp Gly Gly Pro Glu Thr Asp Pro	
260 265 270	
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Ala Ser Thr Met Thr Leu Arg Ile Gly Arg Gly Leu Thr Leu Gln Ile	
275 280 285	
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Val Gln Gly Cys Ile Glu Met Gln Thr Thr Asp Val Ile Gly Asn Ser	

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Gly Tyr Met Gln Asp Phe Lys Ser Gly Arg Val Ala Gln Ser Ile Leu
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aga caa gca ggg gtt gaa atg gaa aag gaa ctt gac aag gtt aac ctg
1008
Arg Gln Ala Gly Val Glu Met Glu Lys Glu Leu Asp Lys Val Asn Leu
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Ser Thr Asp Tyr Gln Glu Val Trp Val Thr Lys Gly Phe Lys Leu Ser
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Cys Gln Tyr Val Phe His Val Ala Trp His Ser Gln Ile Asn Lys Tyr
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Gln Ile Leu Lys Asp Ala Met Lys Ser Cys Leu Glu Lys Cys Leu Lys
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Pro Asp Ile Asn Ser Ile Ser Phe Pro Ala Leu Gly Thr Gly Leu Met
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Asp Leu Lys Lys Ser Thr Ala Ala Gln Ile Met Phe Glu Glu Val Phe
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1296
Ala Phe Ala Lys Glu His Lys Glu Lys Thr Leu Thr Val Lys Ile Val
          420          425          430

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1344
Ile Phe Pro Val Asp Val Glu Thr Tyr Lys Ile Phe Tyr Ala Glu Met
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aca aaa agg tcc aac gag ctg aat ctc agc ggt aat agt ggt gct tta
1392
Thr Lys Arg Ser Asn Glu Leu Asn Leu Ser Gly Asn Ser Gly Ala Leu
          450          455          460

gcc ctg cag tgg tcc agt ggg gag caa aga aga ggc ggc ctt gaa gct
1440
Ala Leu Gln Trp Ser Ser Gly Glu Gln Arg Arg Gly Gly Leu Glu Ala
465          470          475          480

gga tct cct gcc atc aat ctc atg ggt gta aaa gtg gga gag atg tgt
1488

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Gly Ser Pro Ala Ile Asn Leu Met Gly Val Lys Val Gly Glu Met Cys
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 Glu Ala Gln Glu Trp Ile Glu Arg Leu Leu Val Ser Leu Asp His His
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 1584
 Ile Ile Glu Asn Asn His Ile Leu Tyr Leu Gly Lys Lys Glu His Asp
 515 520 525
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 1632
 Val Leu Ser Glu Leu Gln Thr Ser Thr Arg Val Ser Ile Ser Glu Thr
 530 535 540
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 1680
 Val Ser Pro Arg Thr Ala Thr Leu Glu Ile Lys Gly Pro Gln Ala Asp
 545 550 555 560
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 1728
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 Gln Gly Thr Asn Gln Gln Glu Lys Leu Asp Lys Met Glu Glu Ser Tyr
 595 600 605
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 Lys Lys Gln Phe Glu Lys Cys Gly Leu Trp Val Val Gln Val Glu Gln
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 1968
 Ile Asp Asn Lys Val Leu Leu Ala Ala Phe Gln Glu Lys Lys Lys Met
 645 650 655
 atg gaa gag agg acg cca aag gga tct ggg agc caa agg ttg ttt cag
 2016
 Met Glu Glu Arg Thr Pro Lys Gly Ser Gly Ser Gln Arg Leu Phe Gln
 660 665 670
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2064

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2112

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690 695 700

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2160

Phe Thr Lys Ser Leu Lys Asn Leu Ala Asp Lys Val Lys Lys Thr Ser
705 710 715 720

agc aca gac aag cta atc tat gtg ttt gag gca gaa gta ctc aca ggg
2208

Ser Thr Asp Lys Leu Ile Tyr Val Phe Glu Ala Glu Val Leu Thr Gly
725 730 735

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2256

Ser Phe Cys Gln Gly Asn Ser Ser Asn Ile Ile Pro Pro Pro Leu Ser
740 745 750

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2304

Pro Gly Ala Leu Asp Val Asn Asp Ser Val Val Asp Asn Val Ser Ser
755 760 765

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2352

Pro Glu Thr Ile Val Val Phe Asn Gly Met Gln Ala Met Pro Leu Tyr
770 775 780

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2400

Leu Trp Thr Cys Thr Gln Asp Arg Thr Phe Ser Gln His Pro Met Trp
785 790 795 800

tca cag gac tac tca tca gga cca gga atg gtc tct tcg ctg cag tcc
2448

Ser Gln Asp Tyr Ser Ser Gly Pro Gly Met Val Ser Ser Leu Gln Ser
805 810 815

tgg gaa tgg gtc tta aat ggc agc tct gtt
2478

Trp Glu Trp Val Leu Asn Gly Ser Ser Val
820 825